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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=7; day=10; hr=16; min=7; sec=19; ms=215;]

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Reviewer Comments:

<210> 52

<211> 0

<212> PRT

<213> Homo sapiens

<400> 52

<210> 53

<211> 0

<212> PRT

<213> Homo sapiens

<400> 53

Per the above, sequence id# 52 and 53 is invalid, no amino acid codings appear. Please also insert mandatory responses for numeric identifier <211> for both sequences. Please check the remaining sequences for similar errors.

Application No: 10573944 Version No: 1.0

Input Set:

Output Set:

Started: 2008-06-05 16:42:23.903
Finished: 2008-06-05 16:42:25.480
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 577 ms
Total Warnings: 0
Total Errors: 2
No. of SeqIDs Defined: 97
Actual SeqID Count: 97

Error code	Error Description
E 106	No body found in 400 Tag SEQID (52)
E 106	No body found in 400 Tag SEQID (53)

SEQUENCE LISTING

<110> Varner, Judith

<120> Methods for Altering Hematopoietic Progenitor Cell Adhesion,
Differentiation, and Migration

<130> UCSD-10834

<140> 10573944

<141> 2008-06-05

<160> 97

<170> PatentIn version 3.3

<210> 1

<211> 1032

<212> PRT

<213> Homo sapiens

<400> 1

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Arg	Glu	Thr	Val	Met	Leu	Leu	Leu	Cys	Leu	Gly	Val	Pro	Thr	Gly	Arg
			20					25						30	

Pro	Tyr	Asn	Val	Asp	Thr	Glu	Ser	Ala	Leu	Leu	Tyr	Gln	Gly	Pro	His
		35						40					45		

Asn	Thr	Leu	Phe	Gly	Tyr	Ser	Val	Val	Leu	His	Ser	His	Gly	Ala	Asn
		50						55					60		

Arg	Trp	Leu	Leu	Val	Gly	Ala	Pro	Thr	Ala	Asn	Trp	Leu	Ala	Asn	Ala
65					70					75				80	

Ser	Val	Ile	Asn	Pro	Gly	Ala	Ile	Tyr	Arg	Cys	Arg	Ile	Gly	Lys	Asn
			85						90					95	

Pro	Gly	Gln	Thr	Cys	Glu	Gln	Leu	Gln	Leu	Gly	Ser	Pro	Asn	Gly	Glu
			100					105						110	

Pro	Cys	Gly	Lys	Thr	Cys	Leu	Glu	Glu	Arg	Asp	Asn	Gln	Trp	Leu	Gly
		115					120					125			

Val	Thr	Leu	Ser	Arg	Gln	Pro	Gly	Glu	Asn	Gly	Ser	Ile	Val	Thr	Cys
		130					135					140			

Gly His Arg Trp Lys Asn Ile Phe Tyr Ile Lys Asn Glu Asn Lys Leu
145 150 155 160

Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro Asp Leu Arg Thr Glu Leu
165 170 175

Ser Lys Arg Ile Ala Pro Cys Tyr Gln Asp Tyr Val Lys Lys Phe Gly
180 185 190

Glu Asn Phe Ala Ser Cys Gln Ala Gly Ile Ser Ser Phe Tyr Thr Lys
195 200 205

Asp Leu Ile Val Met Gly Ala Pro Gly Ser Ser Tyr Trp Thr Gly Ser
210 215 220

Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys Tyr Lys Ala Phe Leu Asp
225 230 235 240

Lys Gln Asn Gln Val Lys Phe Gly Ser Tyr Leu Gly Tyr Ser Val Gly
245 250 255

Ala Gly His Phe Arg Ser Gln His Thr Thr Glu Val Val Gly Gly Ala
260 265 270

Pro Gln His Glu Gln Ile Gly Lys Ala Tyr Ile Phe Ser Ile Asp Glu
275 280 285

Lys Glu Leu Asn Ile Leu His Glu Met Lys Gly Lys Lys Leu Gly Ser
290 295 300

Tyr Phe Gly Ala Ser Val Cys Ala Val Asp Leu Asn Ala Asp Gly Phe
305 310 315 320

Ser Asp Leu Leu Val Gly Ala Pro Met Gln Ser Thr Ile Arg Glu Glu
325 330 335

Gly Arg Val Phe Val Tyr Ile Asn Ser Gly Ser Gly Ala Val Met Asn
340 345 350

Ala Met Glu Thr Asn Leu Val Gly Ser Asp Lys Tyr Ala Ala Arg Phe
355 360 365

Gly	Glu	Ser	Ile	Val	Asn	Leu	Gly	Asp	Ile	Asp	Asn	Asp	Gly	Phe	Glu	370	375	380	
Asp	Val	Ala	Ile	Gly	Ala	Pro	Gln	Glu	Asp	Asp	Leu	Gln	Gly	Ala	Ile	385	390	395	400
Tyr	Ile	Tyr	Asn	Gly	Arg	Ala	Asp	Gly	Ile	Ser	Ser	Thr	Phe	Ser	Gln	405	410	415	
Arg	Ile	Glu	Gly	Leu	Gln	Ile	Ser	Lys	Ser	Leu	Ser	Met	Phe	Gly	Gln	420	425	430	
Ser	Ile	Ser	Gly	Gln	Ile	Asp	Ala	Asp	Asn	Asn	Gly	Tyr	Val	Asp	Val	435	440	445	
Ala	Val	Gly	Ala	Phe	Arg	Ser	Asp	Ser	Ala	Val	Leu	Leu	Arg	Thr	Arg	450	455	460	
Pro	Val	Val	Ile	Val	Asp	Ala	Ser	Leu	Ser	His	Pro	Glu	Ser	Val	Asn	465	470	475	480
Arg	Thr	Lys	Phe	Asp	Cys	Val	Glu	Asn	Gly	Trp	Pro	Ser	Val	Cys	Ile	485	490	495	
Asp	Leu	Thr	Leu	Cys	Phe	Ser	Tyr	Lys	Gly	Lys	Glu	Val	Pro	Gly	Tyr	500	505	510	
Ile	Val	Leu	Phe	Tyr	Asn	Met	Ser	Leu	Asp	Val	Asn	Arg	Lys	Ala	Glu	515	520	525	
Ser	Pro	Pro	Arg	Phe	Tyr	Phe	Ser	Ser	Asn	Gly	Thr	Ser	Asp	Val	Ile	530	535	540	
Thr	Gly	Ser	Ile	Gln	Val	Ser	Ser	Arg	Glu	Ala	Asn	Cys	Arg	Thr	His	545	550	555	560
Gln	Ala	Phe	Met	Arg	Lys	Asp	Val	Arg	Asp	Ile	Leu	Thr	Pro	Ile	Gln	565	570	575	
Ile	Glu	Ala	Ala	Tyr	His	Leu	Gly	Pro	His	Val	Ile	Ser	Lys	Arg	Ser	580	585	590	

Thr Glu Glu Phe Pro Pro Leu Gln Pro Ile Leu Gln Gln Lys Lys Glu
595 600 605

Lys Asp Ile Met Lys Lys Thr Ile Asn Phe Ala Arg Phe Cys Ala His
610 615 620

Glu Asn Cys Ser Ala Asp Leu Gln Val Ser Ala Lys Ile Gly Phe Leu
625 630 635 640

Lys Pro His Glu Asn Lys Thr Tyr Leu Ala Val Gly Ser Met Lys Thr
645 650 655

Leu Met Leu Asn Val Ser Leu Phe Asn Ala Gly Asp Asp Ala Tyr Glu
660 665 670

Thr Thr Leu His Val Lys Leu Pro Val Gly Leu Tyr Phe Ile Lys Ile
675 680 685

Leu Glu Leu Glu Glu Lys Gln Ile Asn Cys Glu Val Thr Asp Asn Ser
690 695 700

Gly Val Val Gln Leu Asp Cys Ser Ile Gly Tyr Ile Tyr Val Asp His
705 710 715 720

Leu Ser Arg Ile Asp Ile Ser Phe Leu Leu Asp Val Ser Ser Leu Ser
725 730 735

Arg Ala Glu Glu Asp Leu Ser Ile Thr Val His Ala Thr Cys Glu Asn
740 745 750

Glu Glu Glu Met Asp Asn Leu Lys His Ser Arg Val Thr Val Ala Ile
755 760 765

Pro Leu Lys Tyr Glu Val Lys Leu Thr Val His Gly Phe Val Asn Pro
770 775 780

Thr Ser Phe Val Tyr Gly Ser Asn Asp Glu Asn Glu Pro Glu Thr Cys
785 790 795 800

Met Val Glu Lys Met Asn Leu Thr Phe His Val Ile Asn Thr Gly Asn
805 810 815

Ser Met Ala Pro Asn Val Ser Val Glu Ile Met Val Pro Asn Ser Phe

820

825

830

Ser Pro Gln Thr Asp Lys Leu Phe Asn Ile Leu Asp Val Gln Thr Thr
835 840 845

Thr Gly Glu Cys His Phe Glu Asn Tyr Gln Arg Val Cys Ala Leu Glu
850 855 860

Gln Gln Lys Ser Ala Met Gln Thr Leu Lys Gly Ile Val Arg Phe Leu
865 870 875 880

Ser Lys Thr Asp Lys Arg Leu Leu Tyr Cys Ile Lys Ala Asp Pro His
885 890 895

Cys Leu Asn Phe Leu Cys Asn Phe Gly Lys Met Glu Ser Gly Lys Glu
900 905 910

Ala Ser Val His Ile Gln Leu Glu Gly Arg Pro Ser Ile Leu Glu Met
915 920 925

Asp Glu Thr Ser Ala Leu Lys Phe Glu Ile Arg Ala Thr Gly Phe Pro
930 935 940

Glu Pro Asn Pro Arg Val Ile Glu Leu Asn Lys Asp Glu Asn Val Ala
945 950 955 960

His Val Leu Leu Glu Gly Leu His His Gln Arg Pro Lys Arg Tyr Phe
965 970 975

Thr Ile Val Ile Ile Ser Ser Ser Leu Leu Leu Gly Leu Ile Val Leu
980 985 990

Leu Leu Ile Ser Tyr Val Met Trp Lys Ala Gly Phe Phe Lys Arg Gln
995 1000 1005

Tyr Lys Ser Ile Leu Gln Glu Glu Asn Arg Arg Asp Ser Trp Ser
1010 1015 1020

Tyr Ile Asn Ser Lys Ser Asn Asp Asp
1025 1030

<210> 2

<211> 798

<212> PRT
<213> Homo sapiens

<400> 2

Met Asn Leu Gln Pro Ile Phe Trp Ile Gly Leu Ile Ser Ser Val Cys
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Cys Val Phe Ala Gln Thr Asp Glu Asn Arg Cys Leu Lys Ala Asn Ala
20 25 30

Lys Ser Cys Gly Glu Cys Ile Gln Ala Gly Pro Asn Cys Gly Trp Cys
35 40 45

Thr Asn Ser Thr Phe Leu Gln Glu Gly Met Pro Thr Ser Ala Arg Cys
50 55 60

Asp Asp Leu Glu Ala Leu Lys Lys Lys Gly Cys Pro Pro Asp Asp Ile
65 70 75 80

Glu Asn Pro Arg Gly Ser Lys Asp Ile Lys Lys Asn Lys Asn Val Thr
85 90 95

Asn Arg Ser Lys Gly Thr Ala Glu Lys Leu Lys Pro Glu Asp Ile His
100 105 110

Gln Ile Gln Pro Gln Gln Leu Val Leu Arg Leu Arg Ser Gly Glu Pro
115 120 125

Gln Thr Phe Thr Leu Lys Phe Lys Arg Ala Glu Asp Tyr Pro Ile Asp
130 135 140

Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Glu
145 150 155 160

Asn Val Lys Ser Leu Gly Thr Asp Leu Met Asn Glu Met Arg Arg Ile
165 170 175

Thr Ser Asp Phe Arg Ile Gly Phe Gly Ser Phe Val Glu Lys Thr Val
180 185 190

Met Pro Tyr Ile Ser Thr Thr Pro Ala Lys Leu Arg Asn Pro Cys Thr
195 200 205

Ser Glu Gln Asn Cys Thr Thr Pro Phe Ser Tyr Lys Asn Val Leu Ser
210 215 220

Leu Thr Asn Lys Gly Glu Val Phe Asn Glu Leu Val Gly Lys Gln Arg
225 230 235 240

Ile Ser Gly Asn Leu Asp Ser Pro Glu Gly Gly Phe Asp Ala Ile Met
245 250 255

Gln Val Ala Val Cys Gly Ser Leu Ile Gly Trp Arg Asn Val Thr Arg
260 265 270

Leu Leu Val Phe Ser Thr Asp Ala Gly Phe His Phe Ala Gly Asp Gly
275 280 285

Lys Leu Gly Gly Ile Val Leu Pro Asn Asp Gly Gln Cys His Leu Glu
290 295 300

Asn Asn Met Tyr Thr Met Ser His Tyr Tyr Asp Tyr Pro Ser Ile Ala
305 310 315 320

His Leu Val Gln Lys Leu Ser Glu Asn Asn Ile Gln Thr Ile Phe Ala
325 330 335

Val Thr Glu Glu Phe Gln Pro Val Tyr Lys Glu Leu Lys Asn Leu Ile
340 345 350

Pro Lys Ser Ala Val Gly Thr Leu Ser Ala Asn Ser Ser Asn Val Ile
355 360 365

Gln Leu Ile Ile Asp Ala Tyr Asn Ser Leu Ser Ser Glu Val Ile Leu
370 375 380

Glu Asn Gly Lys Leu Ser Glu Gly Val Thr Ile Ser Tyr Lys Ser Tyr
385 390 395 400

Cys Lys Asn Gly Val Asn Gly Thr Gly Glu Asn Gly Arg Lys Cys Ser
405 410 415

Asn Ile Ser Ile Gly Asp Glu Val Gln Phe Glu Ile Ser Ile Thr Ser
420 425 430

Asn Lys Cys Pro Lys Lys Asp Ser Asp Ser Phe Lys Ile Arg Pro Leu

435

440

445

Gly Phe Thr Glu Glu Val Glu Val Ile Leu Gln Tyr Ile Cys Glu Cys
 450 455 460

Glu Cys Gln Ser Glu Gly Ile Pro Glu Ser Pro Lys Cys His Glu Gly
 465 470 475 480

Asn Gly Thr Phe Glu Cys Gly Ala Cys Arg Cys Asn Glu Gly Arg Val
 485 490 495

Gly Arg His Cys Glu Cys Ser Thr Asp Glu Val Asn Ser Glu Asp Met
 500 505 510

Asp Ala Tyr Cys Arg Lys Glu Asn Ser Ser Glu Ile Cys Ser Asn Asn
 515 520 525

Gly Glu Cys Val Cys Gly Gln Cys Val Cys Arg Lys Arg Asp Asn Thr
 530 535 540

Asn Glu Ile Tyr Ser Gly Lys Phe Cys Glu Cys Asp Asn Phe Asn Cys
 545 550 555 560

Asp Arg Ser Asn Gly Leu Ile Cys Gly Gly Asn Gly Val Cys Lys Cys
 565 570 575

Arg Val Cys Glu Cys Asn Pro Asn Tyr Thr Gly Ser Ala Cys Asp Cys
 580 585 590

Ser Leu Asp Thr Ser Thr Cys Glu Ala Ser Asn Gly Gln Ile Cys Asn
 595 600 605

Gly Arg Gly Ile Cys Glu Cys Gly Val Cys Lys Cys Thr Asp Pro Lys
 610 615 620

Phe Gln Gly Gln Thr Cys Glu Met Cys Gln Thr Cys Leu Gly Val Cys
 625 630 635 640

Ala Glu His Lys Glu Cys Val Gln Cys Arg Ala Phe Asn Lys Gly Glu
 645 650 655

Lys Lys Asp Thr Cys Thr Gln Glu Cys Ser Tyr Phe Asn Ile Thr Lys
 660 665 670

Val Glu Ser Arg Asp Lys Leu Pro Gln Pro Val Gln Pro Asp Pro Val
675 680 685

Ser His Cys Lys Glu Lys Asp Val Asp Asp Cys Trp Phe Tyr Phe Thr
690 695 700

Tyr Ser Val Asn Gly Asn Asn Glu Val Met Val His Val Val Glu Asn
705 710 715 720

Pro Glu Cys Pro Thr Gly Pro Asp Ile Ile Pro Ile Val Ala Gly Val
725 730 735

Val Ala Gly Ile Val Leu Ile Gly Leu Ala Leu Leu Leu Ile Trp Lys
740 745 750

Leu Leu Met Ile Ile His Asp Arg Arg Glu Phe Ala Lys Phe Glu Lys
755 760 765

Glu Lys Met Asn Ala Lys Trp Asp Thr Gly Glu Asn Pro Ile Tyr Lys
770 775 780

Ser Ala Val Thr Thr Val Val Asn Pro Lys Tyr Glu Gly Lys
785 790 795

<210> 3
<211> 739
<212> PRT
<213> Homo sapiens

<400> 3

Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp
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Ile Met Phe Ala Ala Ser Gln Ala Phe Lys Ile Glu Thr Thr Pro Glu
20 25 30

Ser Arg Tyr Leu Ala Gln Ile Gly Asp Ser Val Ser Leu Thr Cys Ser
35 40 45

Thr Thr Gly Cys Glu Ser Pro Phe Phe Ser Trp Arg Thr Gln Ile Asp
50 55 60

Ser Pro Leu Asn Gly Lys Val Thr Asn Glu Gly Thr Thr Ser Thr Leu
65 70 75 80

Thr Met Asn Pro Val Ser Phe Gly Asn Glu His Ser Tyr Leu Cys Thr
85 90 95

Ala Thr Cys Glu Ser Arg Lys Leu Glu Lys Gly Ile Gln Val Glu Ile
100 105 110

Tyr Ser Phe Pro Lys Asp Pro Glu Ile His Leu Ser Gly Pro Leu Glu
115 120 125

Ala Gly Lys Pro Ile Thr Val Lys Cys Ser Val Ala Asp Val Tyr Pro
130 135 140

Phe Asp Arg Leu Glu Ile Asp Leu Leu Lys Gly Asp His Leu Met Lys
145 150 155 160

Ser Gln Glu Phe Leu Glu Asp Ala Asp Arg Lys Ser Leu Glu Thr Lys
165 170 175

Ser Leu Glu Val Thr Phe Thr Pro Val Ile Glu Asp Ile Gly Lys Val
180 185 190